Supplementary Table 11. The number of protein-coding genes supported by de novo, transcriptome data and homology prediction.

	>=20% overlap		>=50% overlap		>=80% overlap	
	No.	Ratio (%)	No.	Ratio (%)	No.	Ratio (%)
R	7,429	15.62%	5,549	17.97%	8,627	27.94%
H(single)	57	0.18%	80	0.26%	118	0.38%
H(more)	90	0.29%	125	0.40%	180	0.58%
P(single)	75	0.24%	270	0.87%	880	2.85%
P(more)	17	0.06%	36	0.12%	104	0.34%
HR	10,035	32.50%	10,096	32.70%	8,768	28.40%
PR	3,594	11.64%	3,628	11.75%	3,901	12.63%
PH	521	1.69%	629	2.04%	686	2.22%
PHR	1,140	37.70%	10,363	33.56%	6,907	22.37%
Total	30,853	99.93%	30,776	99.68%	30,171	97.72%